SEQUENCE LISTING

<110> Genetics Institute
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       Twine, Natalie
       Agostino, Michael
       LaVallie, Edward
       Corcoran, Christopher

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<141> 2002-01-25

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Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys Leu
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Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser Gly
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Glu Tyr Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr
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Ala Gly Arg Glu Leu Leu Phe Pro Leu Thr Lys Gly His Ala Ser Lys
                  85                    90                    95
Arg Phe His Pro Arg Ala His Ser Ser Val Pro Pro Pro Pro Gly Val
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His Pro Gly Thr Glu Pro Gly Leu Ser Arg Ala Leu Ser Gln Arg Met
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Gly His Pro Arg Asn Ala His Leu Gly Leu Tyr Tyr Ser Ala Asn Glu
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Arg Glu His Leu Val Ser Leu Pro Ala Val Ala Trp Asp Trp Leu Xaa
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Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val Trp
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gggccccagg aaaactcagt gcagtccagt gcctgtggca ggcagcacct tgagccaaca   3600
ggaaccattg acatgcgagg cccagggcag gcagactgtg cagtggccat ggggcggccc   3660
ctcggggagg tggtgaccct ccgcgtcctt gagagttctc tcaactgcag tgcggggac   3720
atgttgctgc tttggggccg gctcacctgg aggaagatgt gcaggaagct gttggacatg   3780
actttcagct ccaagaccaa cacgctggtg gtgaggcagc gctgcgggcg gccaggaggt   3840
ggggtgctgc tgcggtatgg gagccagctt gctcctgaaa ccttctacag agaatgtgac   3900
atgcagctct ttgggccctg gggtgaaatc gtgagcccct cgctgagtcc agccacgagt   3960
aatgcagggg gctgccggct cttcattaat gtggctccgc acgcacggat tgccatccat   4020
gccctggcca ccaacatggg cgctgggacc gagggagcca atgccagcta catcttgatc   4080
cgggacaccc acagcttgag gaccacagcg ttccatgggc agcaggtgct ctactgggag   4140
tcagagagca gccaggctga gatggagttc agcgagggct tcctgaaggc tcaggccagc   4200
ctgcggggcc agtactggac cctccaatca tgggtaccgg agatgcagga ccctcagtcc   4260
tggaagggaa aggaaggaac ctga                                          4284
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<210>   8
<211>   1427
<212>   PRT
<213>   homo sapiens

<400>   8

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Met His Gln Arg His Pro Trp Ala Arg Cys Pro Pro Leu Cys Val Ala
1               5                   10                  15
Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20                  25                  30
Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
```

```
              35                     40                     45
Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50                      55.                    60
Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                       70                   75                    80.
His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                    85                   90                   95
Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                  105                  110
Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
            115                  120                  125
Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                  135                  140
Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                  150                  155                  160
Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                  170                  175
Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                  185                  190
Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
            195                  200                  205
Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                  215                  220
Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                  230                  235                  240
Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                  250                  255
Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                  265                  270
Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro
    275                  280                  285
Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr
    290                  295                  300
Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val
305                  310                  315                  320
Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser
                325                  330                  335
Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val
            340                  345                  350
Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys
    355                  360                  365
Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His
    370                  375                  380
Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys
385                  390                  395                  400
Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro
                405                  410                  415
Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met
            420                  425                  430
Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln
            435                  440                  445
Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly
    450                  455                  460
Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp
465                  470                  475                  480
Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met
                485                  490                  495
Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly
            500                  505                  510
Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg
    515                  520                  525
```

9

```
Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg
    530                 535                 540
Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly
545                 550                 555                 560
Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val
                565                 570                 575
Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe
            580                 585                 590
Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys
        595                 600                 605
Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly
    610                 615                 620
Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu
625                 630                 635                 640
Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln
            645                 650                 655
Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp
            660                 665                 670
Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp
        675                 680                 685
Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg
        690                 695                 700
Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
705                 710                 715                 720
Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala
                725                 730                 735
Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly
            740                 745                 750
Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val Arg
        755                 760                 765
Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg
    770                 775                 780
Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys Asn
785                 790                 795                 800
Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys
                805                 810                 815
Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val
            820                 825                 830
Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser
        835                 840                 845
Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys
    850                 855                 860
Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala
865                 870                 875                 880
Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val
                885                 890                 895
Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu
            900                 905                 910
Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val
        915                 920                 925
Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu
    930                 935                 940
Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala
945                 950                 955                 960
Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr
                965                 970                 975
Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp
            980                 985                 990
Thr Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu Ala Cys Ser
        995                 1000                1005
Leu Glu Pro Cys Pro Pro Arg Trp Lys Val Met Ser Leu Gly Pro
```

```
        1010                    1015                    1020
Cys Ser Ala Ser Cys Gly Leu Gly Thr Ala Arg Arg Ser Val Ala
        1025                    1030                    1035
Cys Val Gln Leu Asp Gln Gly Gln Asp Val Glu Val Asp Glu Ala
        1040                    1045                    1050
Ala Cys Ala Ala Leu Val Arg Pro Glu Ala Ser Val Pro Cys Leu
        1055                    1060                    1065
Ile Ala Asp Cys Thr Tyr Arg Trp His Val Gly Thr Trp Met Glu
        1070                    1075                    1080
Cys Ser Val Ser Cys Gly Asp Gly Ile Gln Arg Arg Arg Asp Thr
        1085                    1090                    1095
Cys Leu Gly Pro Gln Ala Gln Ala Pro Val Pro Ala Asp Phe Cys
        1100                    1105                    1110
Gln His Leu Pro Lys Pro Val Thr Val Arg Gly Cys Trp Ala Gly
        1115                    1120                    1125
Pro Cys Val Gly Gln Gly Thr Pro Ser Leu Val Pro His Glu Glu
        1130                    1135                    1140
Ala Ala Ala Pro Gly Arg Thr Thr Ala Thr Pro Ala Gly Ala Ser
        1145                    1150                    1155
Leu Glu Trp Ser Gln Ala Arg Gly Leu Leu Phe Ser Pro Ala Pro
        1160                    1165                    1170
Gln Pro Arg Arg Leu Leu Pro Gly Pro Gln Glu Asn Ser Val Gln
        1175                    1180                    1185
Ser Ser Ala Cys Gly Arg Gln His Leu Glu Pro Thr Gly Thr Ile
        1190                    1195                    1200
Asp Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val Ala Ile Gly
        1205                    1210                    1215
Arg Pro Leu Gly Glu Val Val Thr Leu Arg Val Leu Glu Ser Ser
        1220                    1225                    1230
Leu Asn Cys Ser Ala Gly Asp Met Leu Leu Leu Trp Gly Arg Leu
        1235                    1240                    1245
Thr Trp Arg Lys Met Cys Arg Lys Leu Leu Asp Met Thr Phe Ser
        1250                    1255                    1260
Ser Lys Thr Asn Thr Leu Val Val Arg Gln Arg Cys Gly Arg Pro
        1265                    1270                    1275
Gly Gly Gly Val Leu Leu Arg Tyr Gly Ser Gln Leu Ala Pro Glu
        1280                    1285                    1290
Thr Phe Tyr Arg Glu Cys Asp Met Gln Leu Phe Gly Pro Trp Gly
        1295                    1300                    1305
Glu Ile Val Ser Pro Ser Leu Ser Pro Ala Thr Ser Asn Ala Gly
        1310                    1315                    1320
Gly Cys Arg Leu Phe Ile Asn Val Ala Pro His Ala Arg Ile Ala
        1325                    1330                    1335
Ile His Ala Leu Ala Thr Asn Met Gly Ala Gly Thr Glu Gly Ala
        1340                    1345                    1350
Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His Ser Leu Arg Thr
        1355                    1360                    1365
Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu Ser Glu Ser
        1370                    1375                    1380
Ser Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu Lys Ala Gln
        1385                    1390                    1395
Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser Trp Val Pro
        1400                    1405                    1410
Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu Gly Thr
        1415                    1420                    1425
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<210> 9
<211> 11
<212> PRT
<213> Artificial

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<220>
<223>  Zinc binding signature region

<400>  9

Thr Ala Ala His Glu Leu Gly His Val Lys Phe
1                5                   10


<210>  10
<211>  28
<212>  DNA
<213>  Artificial

<220>
<223>  5' probe

<400>  10
gtgaggttgg ctgtgatatt tggagcac                                        28


<210>  11
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' antisense primer

<400>  11
cgctacctga gcaggctcag cagct                                           25


<210>  12
<211>  26
<212>  DNA
<213>  Artificial

<220>
<223>  5' primer

<400>  12
cccgaagcag ttctgccccg atgttg                                          26


<210>  13
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' probe

<400>  13
acccgagttg tcttcaggct ttgga                                           25


<210>  14
<211>  26
<212>  DNA
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<213>  Artificial

<220>
<223>  5' antisense primer

<400>  14
ctccacgctt catgatgaag ctctcg                                          26


<210>  15
<211>  21
<212>  DNA
<213>  Artificial

<220>
<223>  5' sense primer

<400>  15
gcggcgcctc cttctaccac t                                               21


<210>  16
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' antisense primer

<400>  16
tccgtgtcgt cctcagggtt gatgg                                           25


<210>  17
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' antisense primer

<400>  17
ccctcaggct ctgtcagaat gacca                                           25


<210>  18
<211>  21
<212>  DNA
<213>  Artificial

<220>
<223>  5' sense primer

<400>  18
aggggcctgg ctccgtagat g                                               21


<210>  19
<211>  23
<212>  DNA
<213>  Artificial
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<220>
<223>  5' sense primer

<400>  19
ctgggagccg gcgggaggtc tgc                                              23


<210>  20
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' probe

<400>  20
ccacaggccg tgtcttctta cttga                                            25


<210>  21
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  5' probe

<400>  21
ccatgggccc gggcacaata cagg                                             24


<210>  22
<211>  26
<212>  DNA
<213>  Artificial

<220>
<223>  5' primer

<400>  22
caacatcggg gcagaactgc ttcggg                                           26


<210>  23
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  5' primer

<400>  23
ccatgggccc gggcacaata cagg                                             24


<210>  24
<211>  41
<212>  DNA
<213>  Artificial
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<220>
<223> 5' primer

<400> 24
taaatcgaat tcccaccatg caccagcgtc acccctgggc a   41

<210> 25
<211> 25
<212> DNA
<213> Artificial

<220>
<223> 3' primer

<400> 25
ccacgacata gcgccctccg atcct   25

<210> 26
<211> 26
<212> DNA
<213> Artificial

<220>
<223> 5' primer

<400> 26
caacatcggg gcagaactgc ttcggg   26

<210> 27
<211> 24
<212> DNA
<213> Artificial

<220>
<223> 3' primer

<400> 27
ccatgggccc gggcacaata cagg   24

<210> 28
<211> 21
<212> DNA
<213> Artificial

<220>
<223> 5' primer

<400> 28
aggggcctgg ctccgtagat g   21

<210> 29
<211> 41
<212> DNA
<213> Artificial

<220>

<223> 3' primer

<400> 29
atagtttagc ggccgctcag gttccttcct ttcccttcca g   41

<210> 30
<211> 15
<212> DNA
<213> Artificial

<220>
<223> 5' insert

<400> 30
catgggcagc tcgag   15

<210> 31
<211> 34
<212> DNA
<213> Artificial

<220>
<223> 5' intermediate of pMT21

<400> 31
ctgcaggcga gcctgaattc ctcgagccat catg   34

<210> 32
<211> 68
<212> DNA
<213> Artificial

<220>
<223> 5' adapter

<400> 32
cgaggttaaa aaacgtctag gccccccgaa ccacggggac gtggtttcc tttgaaaaac   60
acgattgc   68